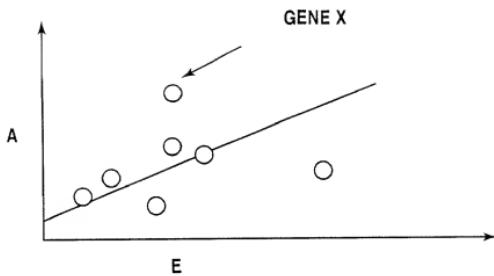
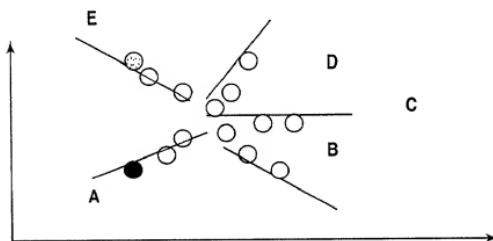


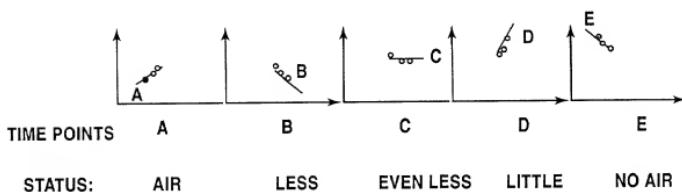
**FIG.1**



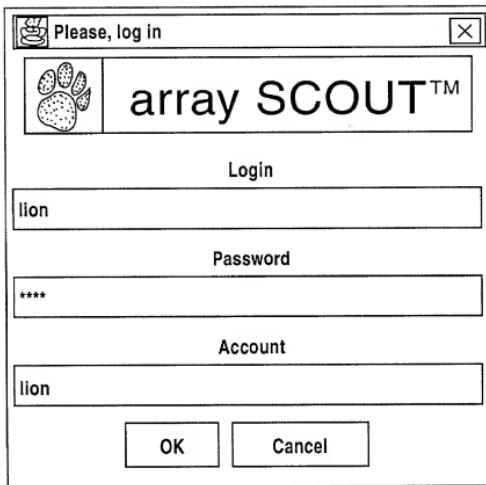
**FIG.2**



**FIG.3**

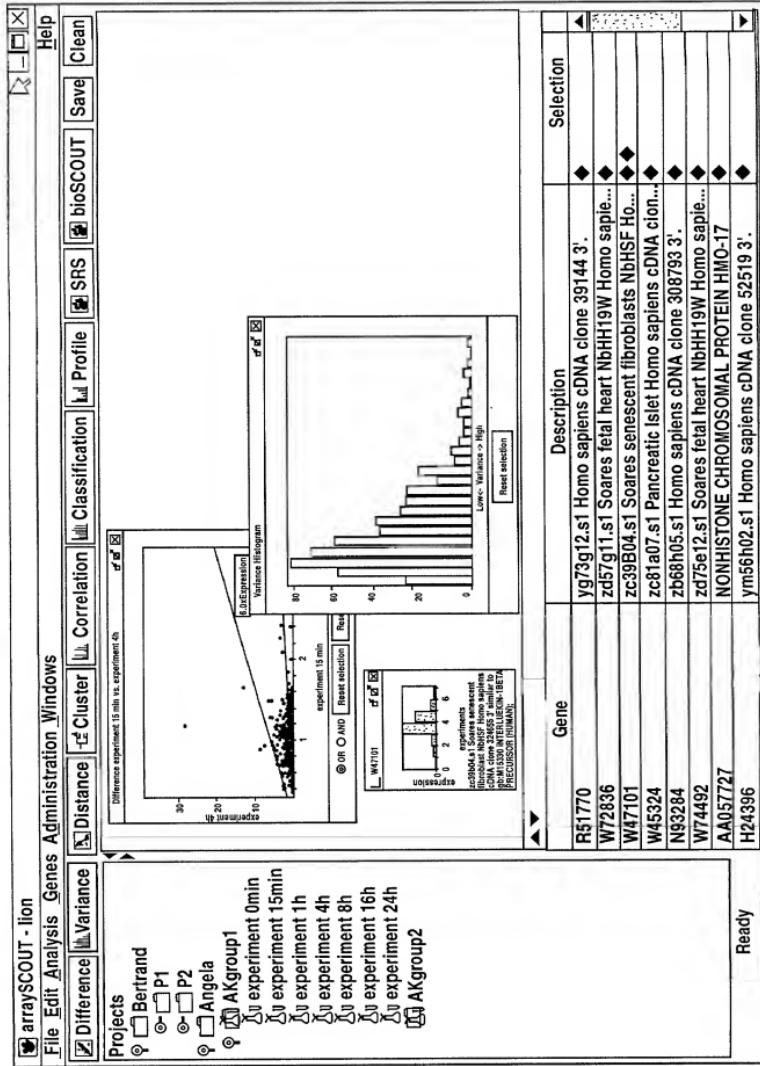


**FIG.4**

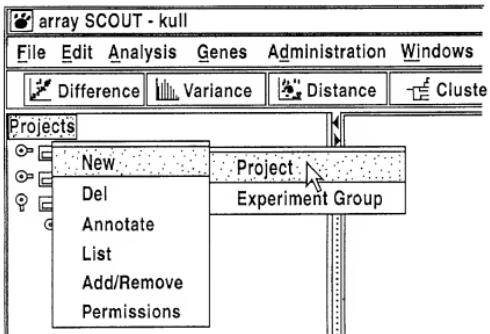


Reich, B. J., & Black, D. H. (1990). Effects of age and sex on the development of spatial skills. *Journal of Cognition and Development*, 1, 13-28.

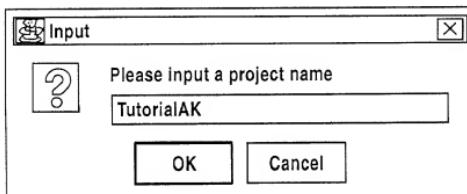
Fig. 5



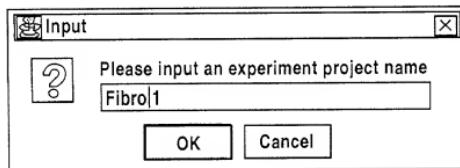
**Fig.6**



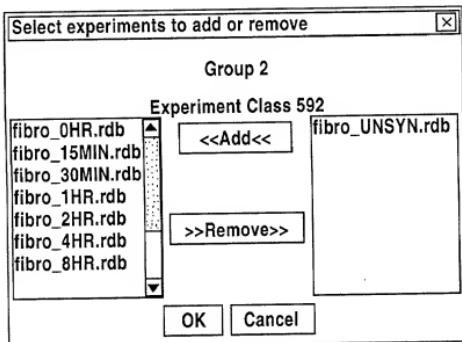
**Fig.7**



**Fig.8**



**Fig.9**



**Fig.10**

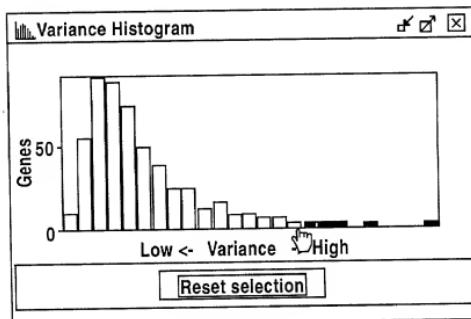


Fig.11

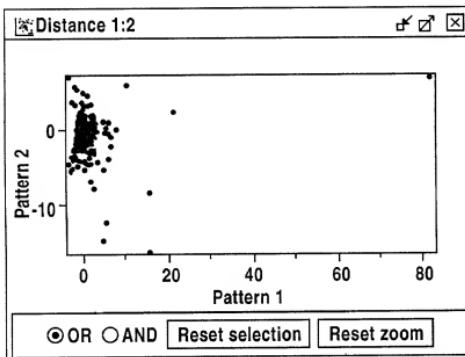


Fig.12

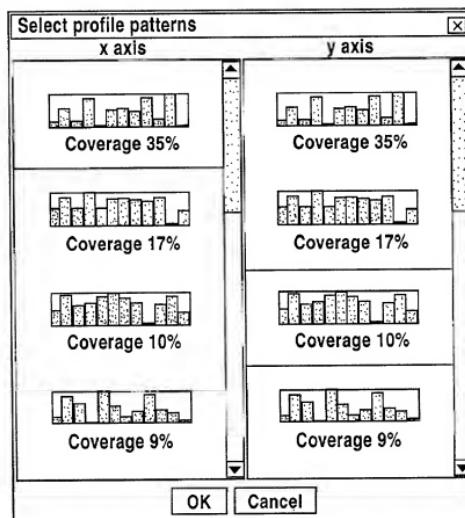


Fig.13

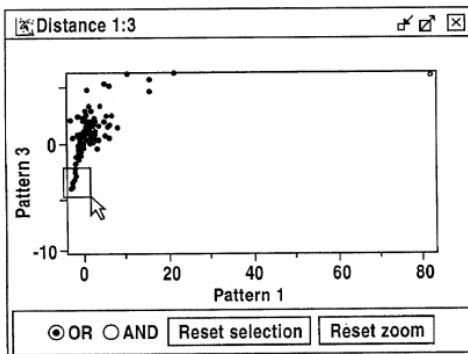
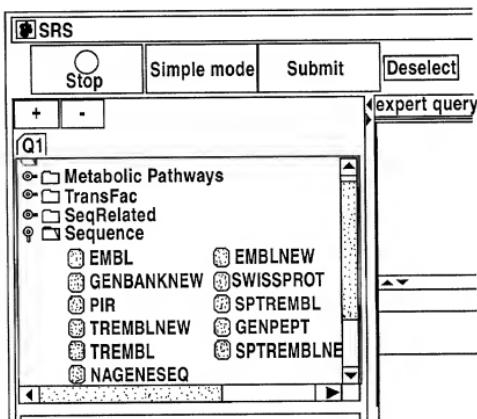


Fig.15



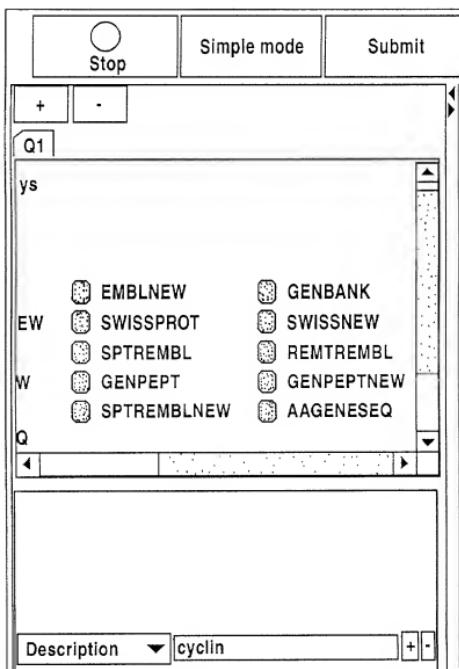
T09000 \* 6241532760

Fig.14

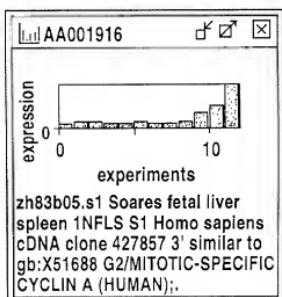
Figure 14 shows a screenshot of a software interface, likely a database or analysis tool, displaying a list of genes. The columns are labeled 'Gene' and 'Description'. A context menu is open over the second row, showing options: 'Select (Ctrl+Enter)', 'Reset selection (Ctrl+R)', and 'Show profile(s) (Ctrl+P)'. The 'Selected in' column contains diamond icons.

Gene	Description	Selected in
W72759	zd71h04.s1 Soares fetal heart NbHH19W Homo sapi...	◆
R40626	yf72g12.s1 Homo sapiens cDNA clone 28051.3.	◆
AA001916	zh83b05.s1 Soares fetal liver spleen NFLS S1:Homo...	◆◆
R43728	yg20c12.s1 Homo sapiens cDNA clone 32811.3.	◆
AA041370	zf09a02.s1 Soares fetal heart NbHH19W Homo sapi...	◆◆
T95837	ye42c02.s1:Homo sapiens cDNA:clone:120346.3	◆◆
H27557	yf61g03.s1 Homo sapiens cDNA:clone:162772.3: simi...	◆◆
AA024572	ze76h08.s1 Soares fetal heart NbHH19W Homo sapi...	◆

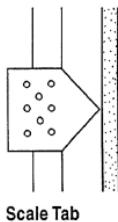
**Fig.16**



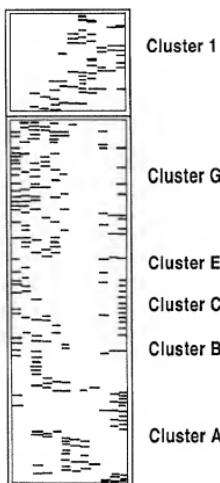
**Fig.17**



**Fig.18**



**Fig.19**



**Fig.20**

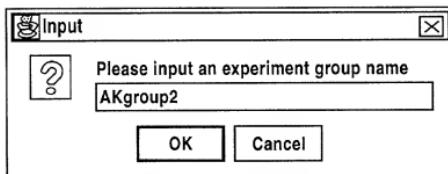
**Projects**

-  Bertrand
-  fibroblast data
-  Fibroblast Project
-  Illico Presto

**Fig.21**

-  **Experiment group 1**
  -  experiment 0 min
  -  experiment 15 min
  -  experiment 30 min
  -  experiment 1h
  -  experiment 2h

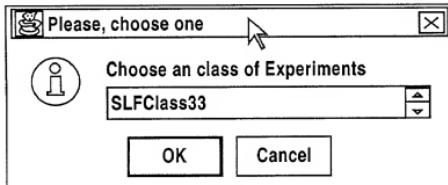
**Fig.22**



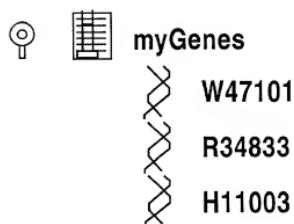
Experiment group name dialog box.

**Fig.23**

Choose experiment class dialog box.

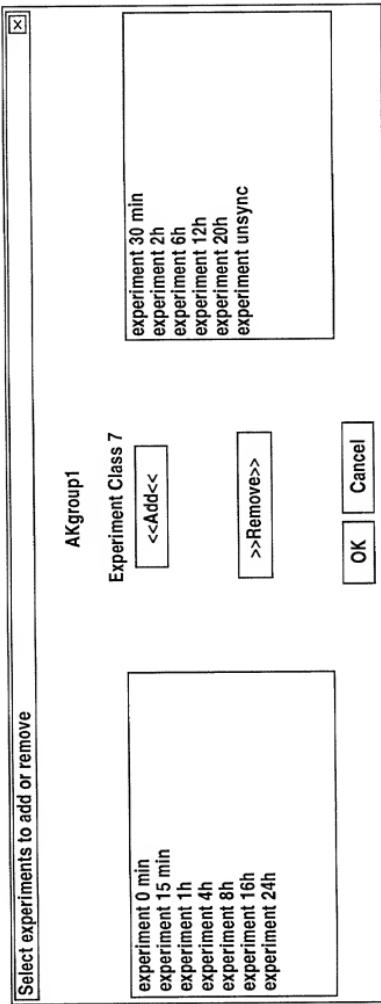


**Fig.25**



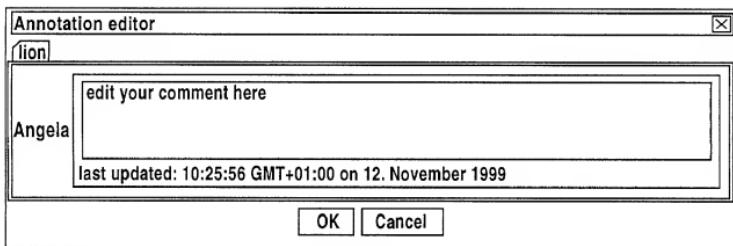
**Fig.24**

Add/Remove dialog box for adding and removing experiments from experiment groups.



## Fig.26

The annotation editor.



## Fig.27

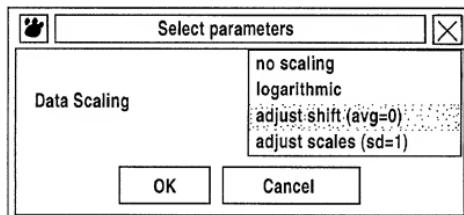
The permissions dialog box for project "Angela".

A screenshot of a Windows-style dialog box titled "Modify permissions for 'Angela'". It shows a table of user permissions. The columns are labeled "User", "READ", "WRITE", "EXECUTE", "Group", "READ", "WRITE", and "EXECUTE". The rows list users: "lion", "weiss", "fabre", "schnecke", "test", "lefranc", and "munro". The "READ" column for "lion" has an "x". The "WRITE" column for "lion" has an "x". The "EXECUTE" column for "lion" has an "x". The "Group" column is empty. The "READ", "WRITE", and "EXECUTE" columns for all other users are empty. At the bottom are two buttons: "OK" and "Cancel".

User	READ	WRITE	EXECUTE	Group	READ	WRITE	EXECUTE
lion	x	x	x				
weiss							
fabre							
schnecke							
test							
lefranc							
munro							

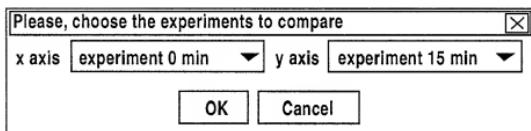
## Fig.28

Select parameters "Data Scaling" dialog box.



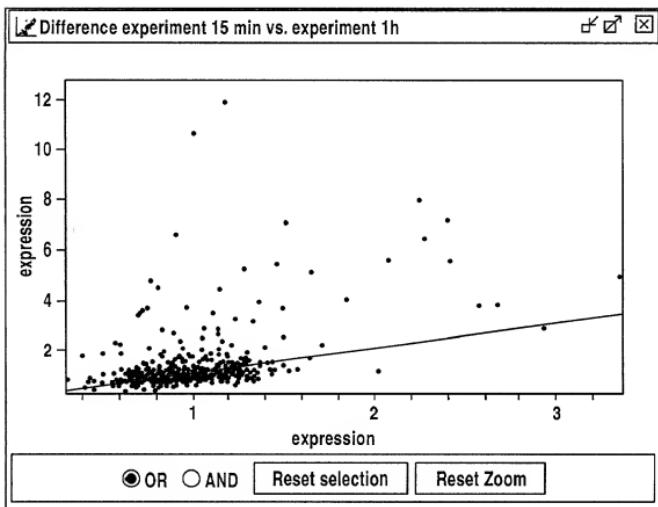
**Fig.29**

The Choose experiments dialog box.



**Fig.30**

An example difference plot.



**Fig.31**

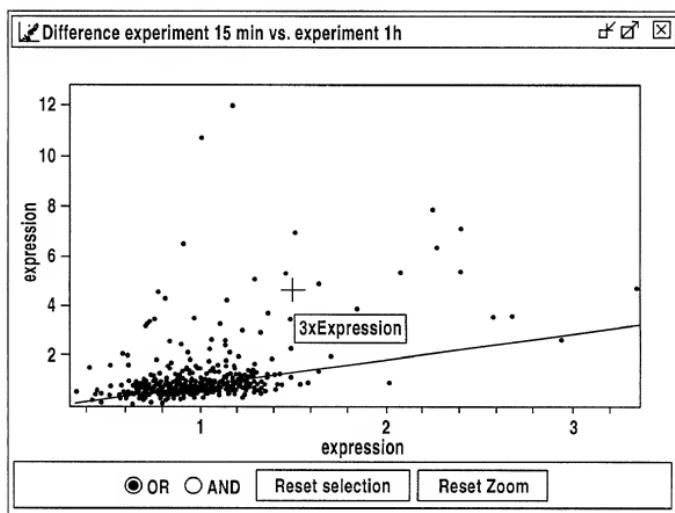
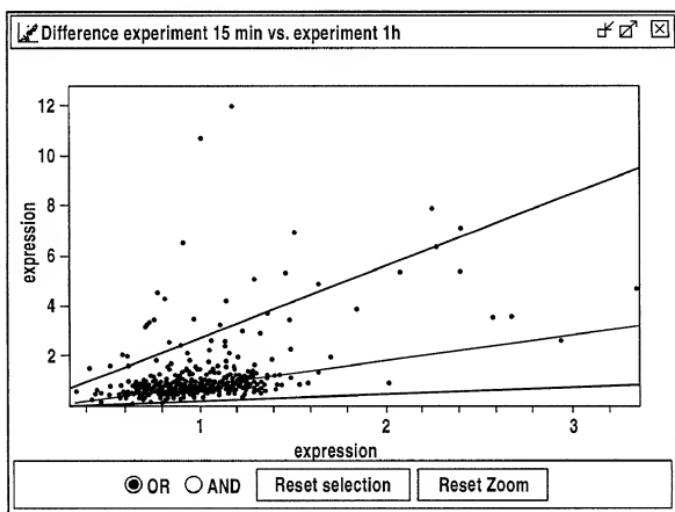
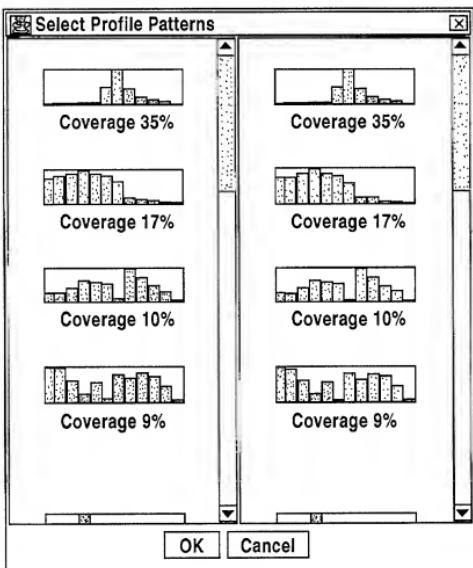


Fig.32



**Fig.33**

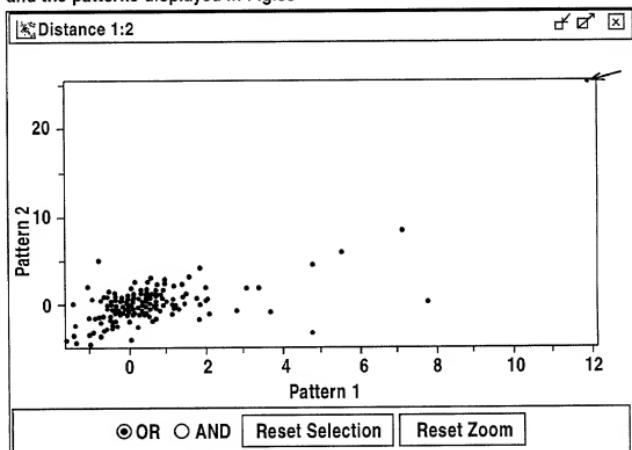
### Select Profile Patterns dialog box.



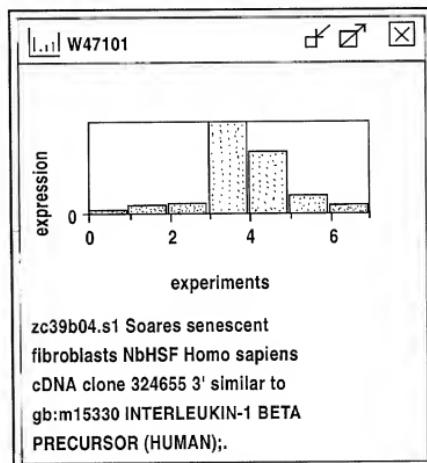
### Fig.34

Gene profiled in Fig.35

Distance Plot created with the adjust shift (avg=0) scaling procedure  
and the patterns displayed in Fig.33



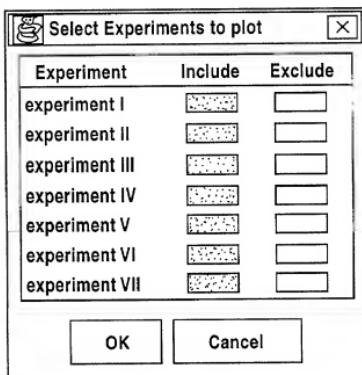
### Fig.35



Gene Profile of gene W47101 plotted at (12,26) in the above Distance Plot (Figure 34).

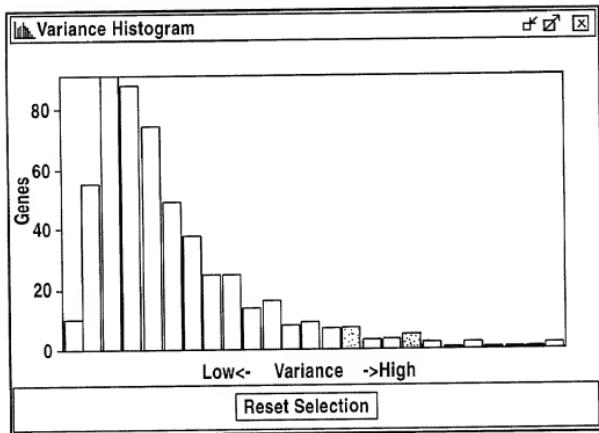
**Fig.36**

The "Select Experiments to plot" dialog box for the variance histogram.



## Fig.37

The Variance Histogram with two bars selected.



## Fig.38

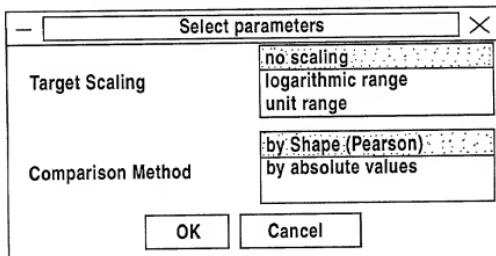
The "Enter Correlation Values" dialog box.

Experiment	Target Value
experiment 0 min	1
experiment 15 min	1
experiment 30 min	1
experiment 1h	1
experiment 2h	1
experiment 8h	1
experiment 6h	1
experiment 8h	1
experiment 12h	10.0
experiment 16h	1
experiment 20h	1
experiment 24h	1

OK Cancel

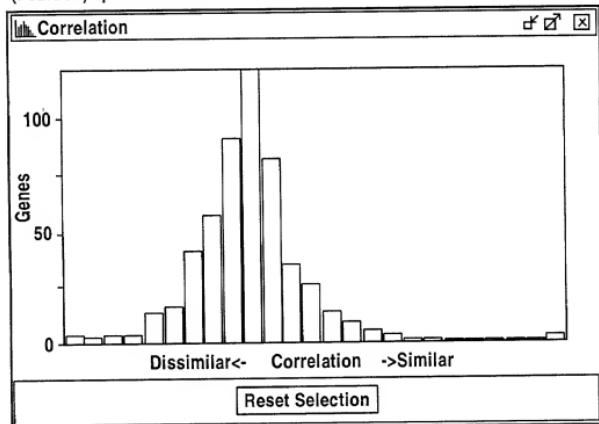
**Fig.39**

Correlation histogram parameters dialog box.



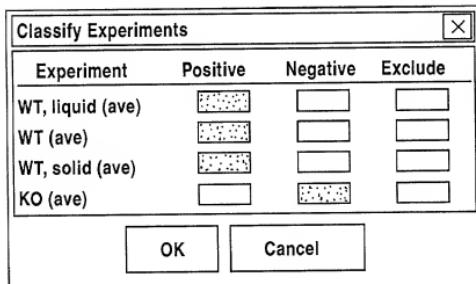
**Fig.40**

A correlation histogram created using the "no scaling" and the "by Shape (Pearson)" parameters.

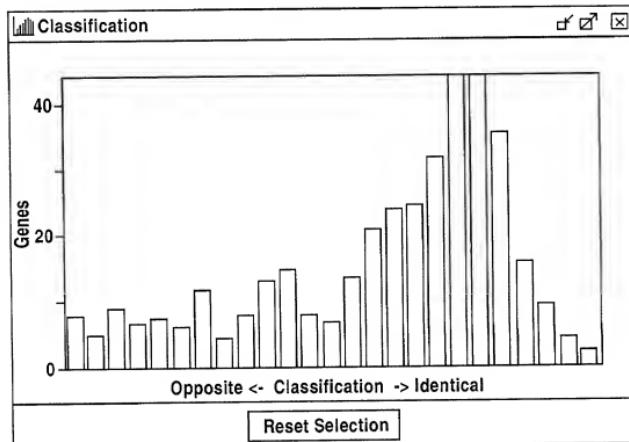


## Fig.41

The "Classify Experiments" dialog box.



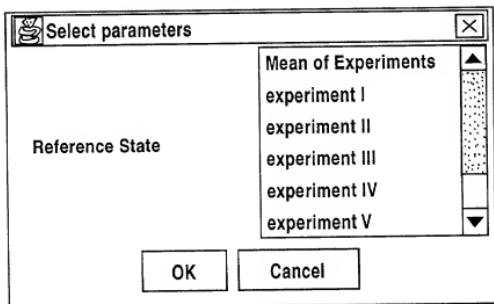
## Fig.42



The Classification histogram created using the "adjust scales" scaling procedure and the data displayed in the "Classify Experiments" dialog box above (Figure 41).

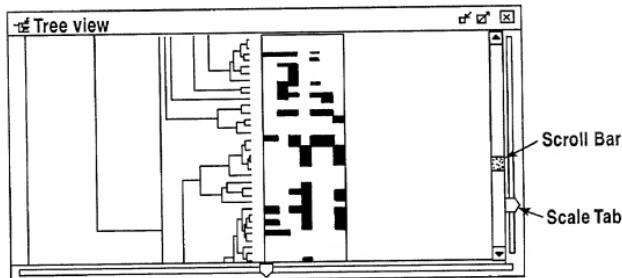
**Fig.43**

Select reference state dialog box.



**Fig.44**

The Cluster Tree analysis view.



**Fig.45**

The SRS interface In Simple Mode.

TOP SECRET//SI//NOFORN

SRS

Stop    Detail mode    **Submit**    Deselect

Query on pathway

Query on swissprot alone

retrieve possible human sequences  
retrieve sequences with nucleotide b  
search mutation database

keyword: **membrane**

Query on swissprot alone

Num	Db	ID	Description
1	SWISSPROT	AC01_YEAST	
2	SWISSPROT	ACR1_YEAST	
3	SWISSPROT	ACR3_YEAST	
4	SWISSPROT	ADB1_YEAST	
	SWISSPROT	ADB2_YEAST	

**BACK**    **FORWARD**

**Fig.46**

The screenshot shows the SRS software interface in Detail Mode. At the top, there is a search bar with the query "Query on swissprot alone". Below the search bar is a table titled "Query on swissprot alone" with columns "Num", "Db", and "ID". The results show entries for various proteins, such as AP17 YEAST, FTR1 YEAST, IM17 YEAST, IM22 YEAST, IM23 YEAST, IM44 YEAST, and IM54 YEAST. Below the table is a URL: [http://bsserver1/srs6bin/cgi-bin/wget?e+!SWISSPROT-ID:IM17\\_YEAST](http://bsserver1/srs6bin/cgi-bin/wget?e+!SWISSPROT-ID:IM17_YEAST). There are "Back" and "Forward" buttons below the URL.

On the left side of the interface, there is a sidebar with several checkboxes: "all dbs", "Metabolic Pathways", "Transfac", "SeqRelated", "Sequence", "EMBL", "EMBLNEW", "GENBANKNEW", "PIR", "TREMBL", "TREMBLNEW", "SWISSPROT", "SPTRIMBL", "GENPEPT", and "SPTRIMBLNEW".

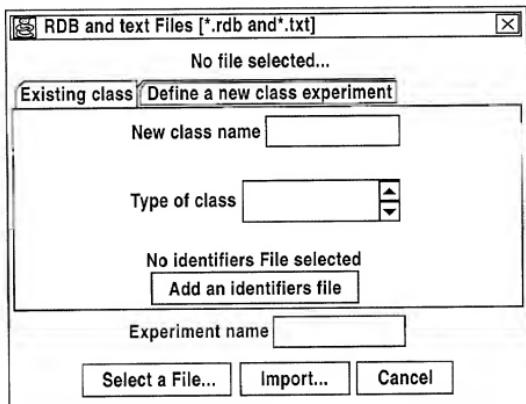
The main panel displays detailed information for the protein "IM17 YEAST". The fields include:

- ID:** IM17 YEAST
- STANDARD:** PRT: 158 AA.
- AC:** P39515; QQ2310;
- DT:** 01-FEB-1995 (Rel. 31, Created)
- DT:** 01-FEB-1995 (Rel. 31, Last sequence update)
- DT:** 15-JUL-1998 (Rel. 36, Last annotation update)
- DE:** MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE S
- DE:** (MITOCHONDRIAL PROTEIN IMPORT PROTEIN 2) (MITOCHO
- DE:** PROTEIN MIN17).
- GM:** IM17.0R MP12.0R MIM17.0R SMS1.0R YJ143W OR J064

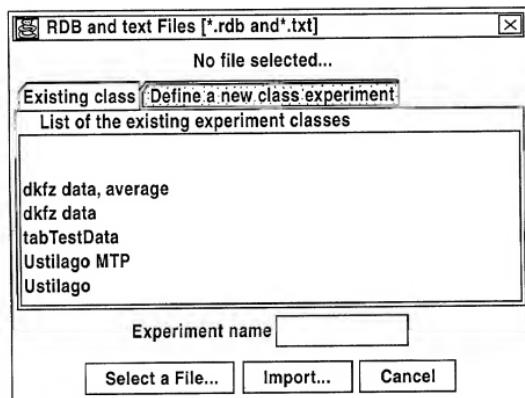
The "Description" field contains the value "membrane".

The software SRS interface in Detail Mode displaying a completed query and a database entry.

**Fig.47**

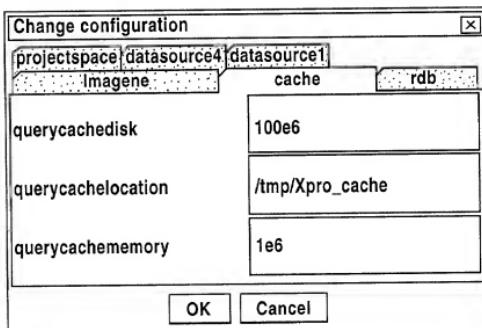


**Fig.48**



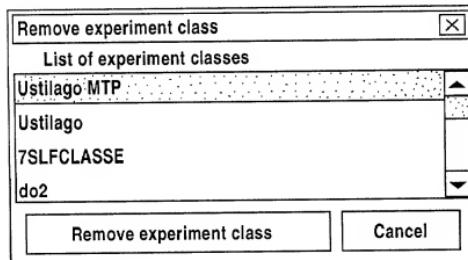
**Fig.49**

Change configuration dialog box.



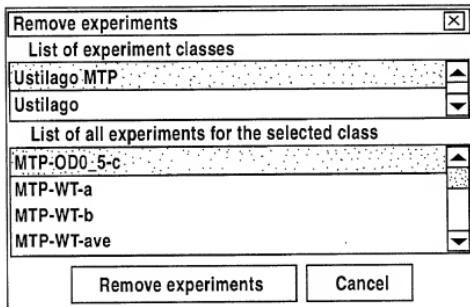
**Fig.50**

Remove experiment class dialog box.



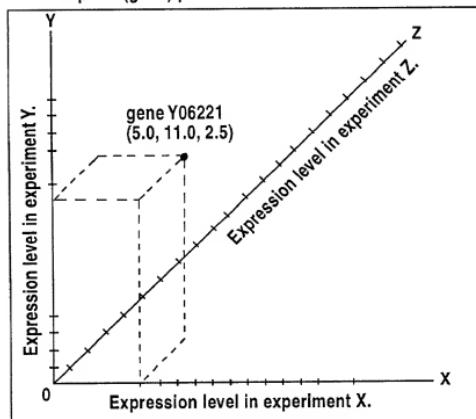
**Fig.51**

Remove experiments dialog box.



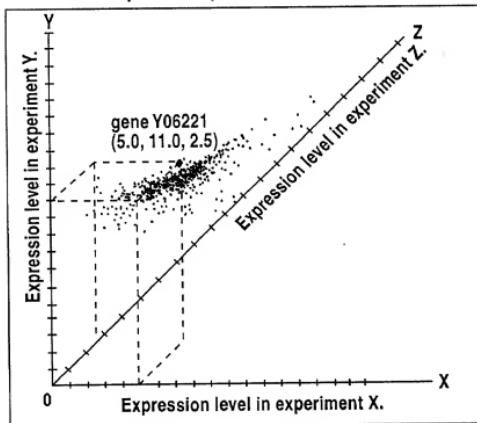
**Fig.52**

A point (gene) plotted in three dimensions.



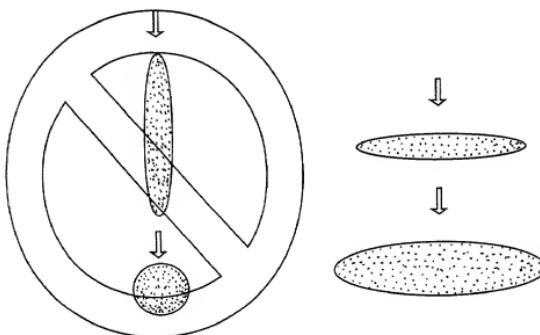
**Fig.53**

Three experiments plotted in 3 dimensions.



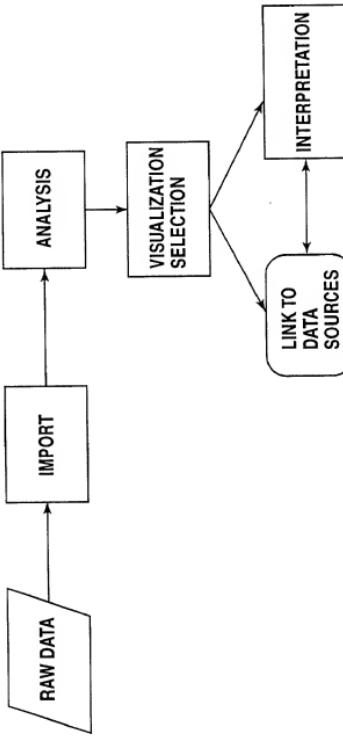
**Fig.54**

Squash the cigar along its side to best preserve its shape.



**FIG.55**

GENERAL FLOW CHART ARRAY ANALYSIS



TO 3030 • 62h59'55"

FIG.56

ANALYSIS OF SEVERAL UNCHARACTERIZED SAMPLES

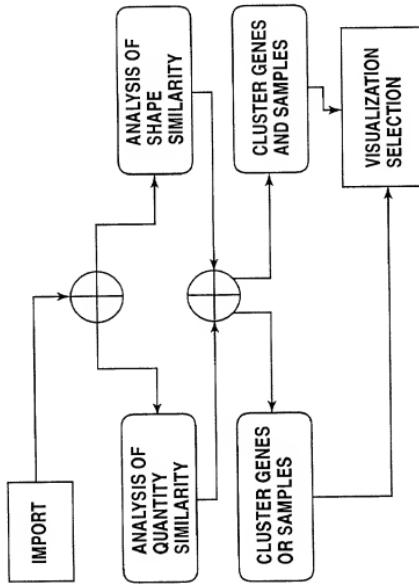


FIG.57

ANALYSIS OF CHARACTERIZED SETS OF SAMPLES

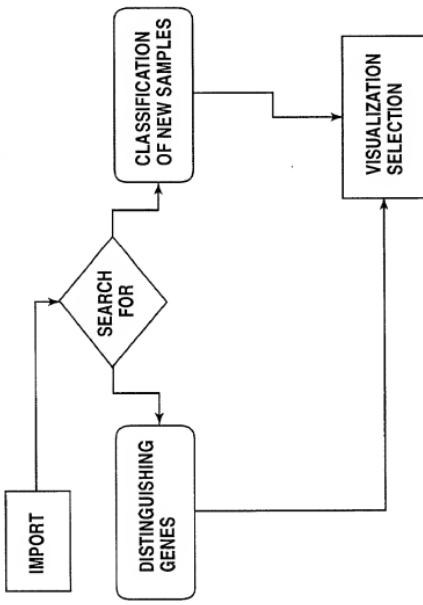
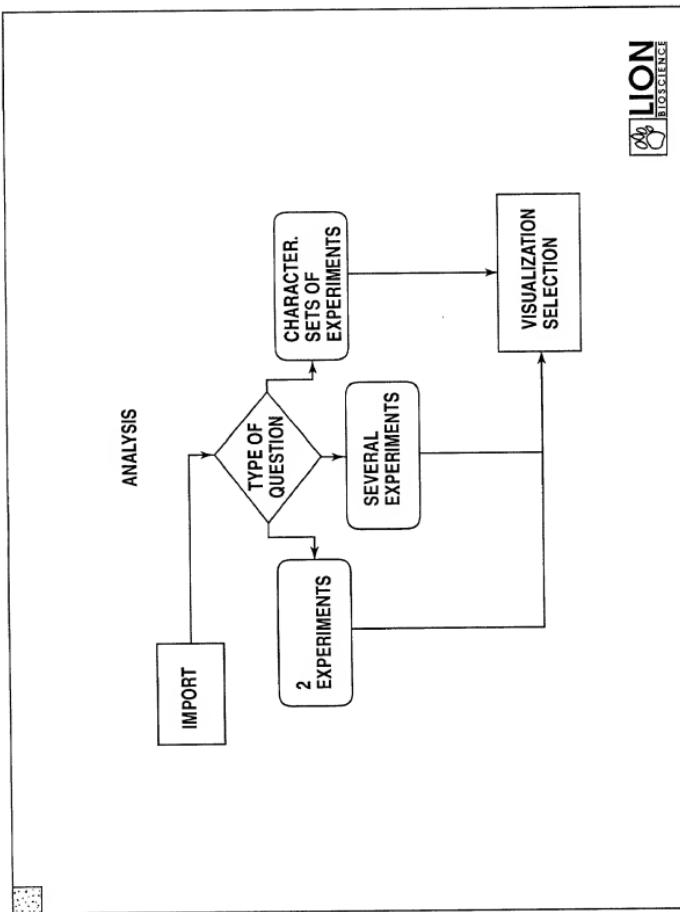


FIG.58



TOSOZO "624153760

FIG.59

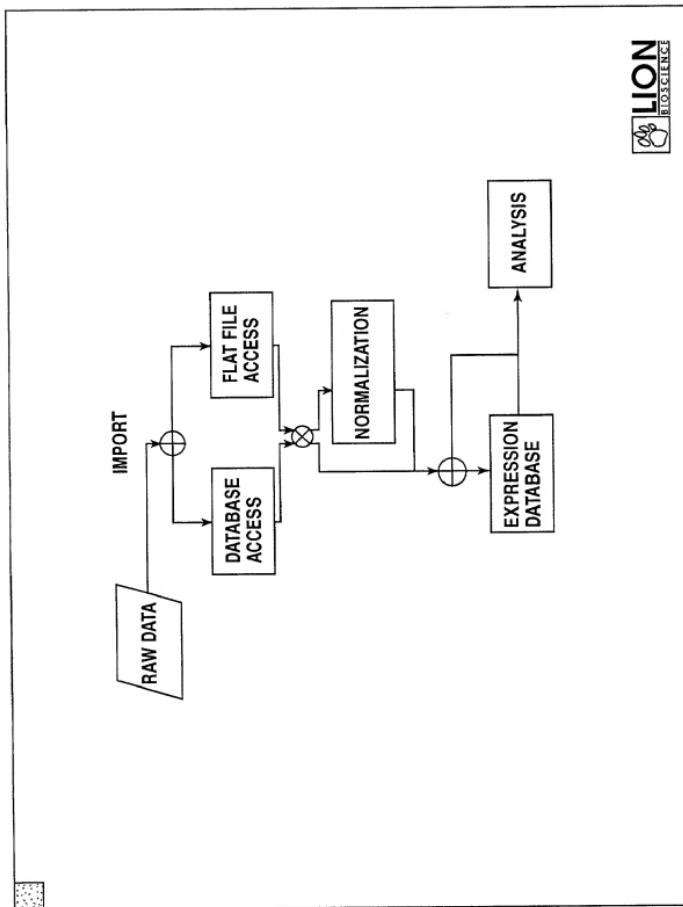
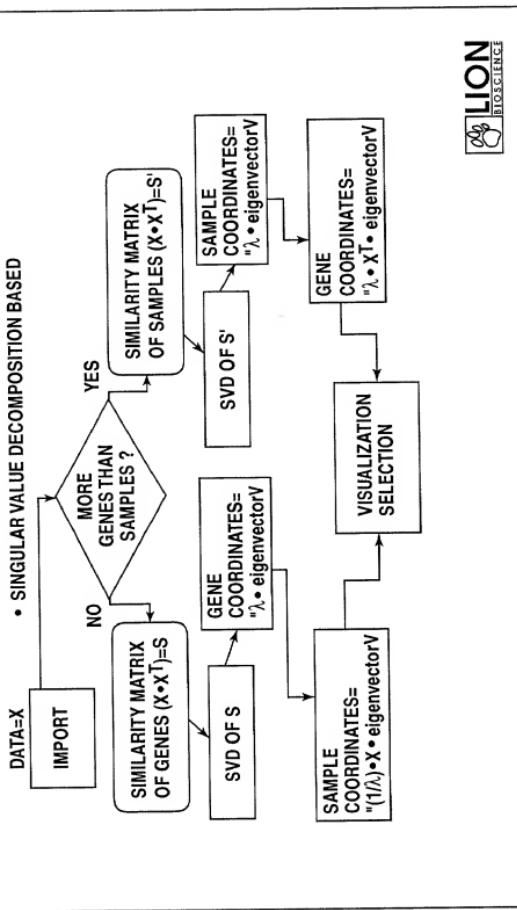


FIG.60

## SIMULTANEOUS ANALYSIS OF GENE AND SAMPLE SIMILARITY



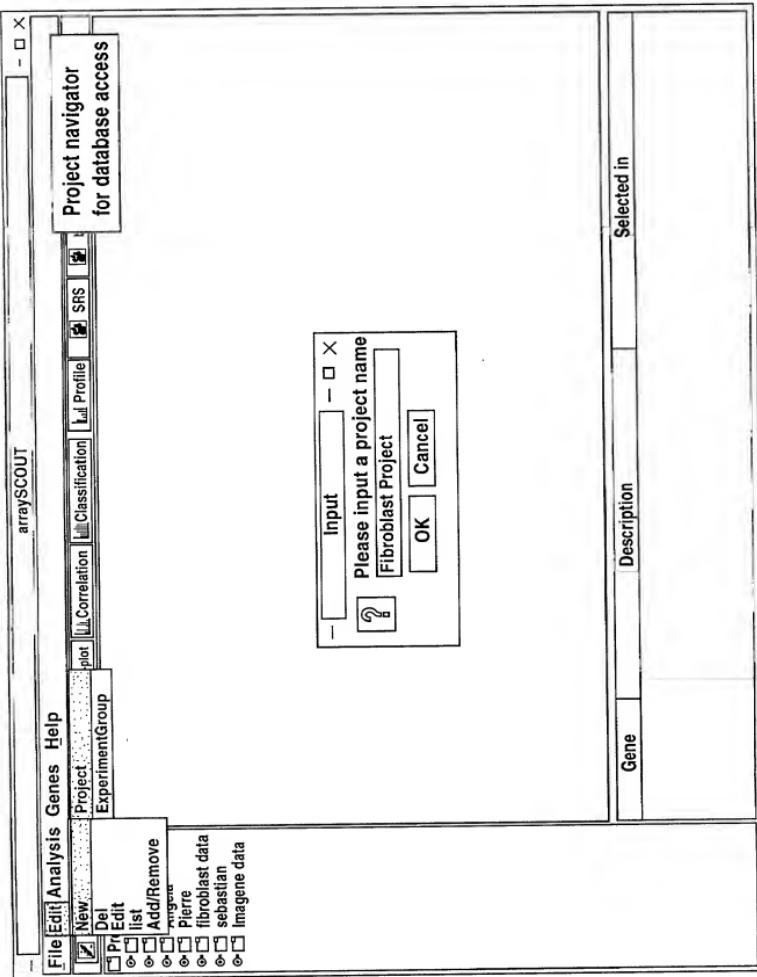


FIG.61

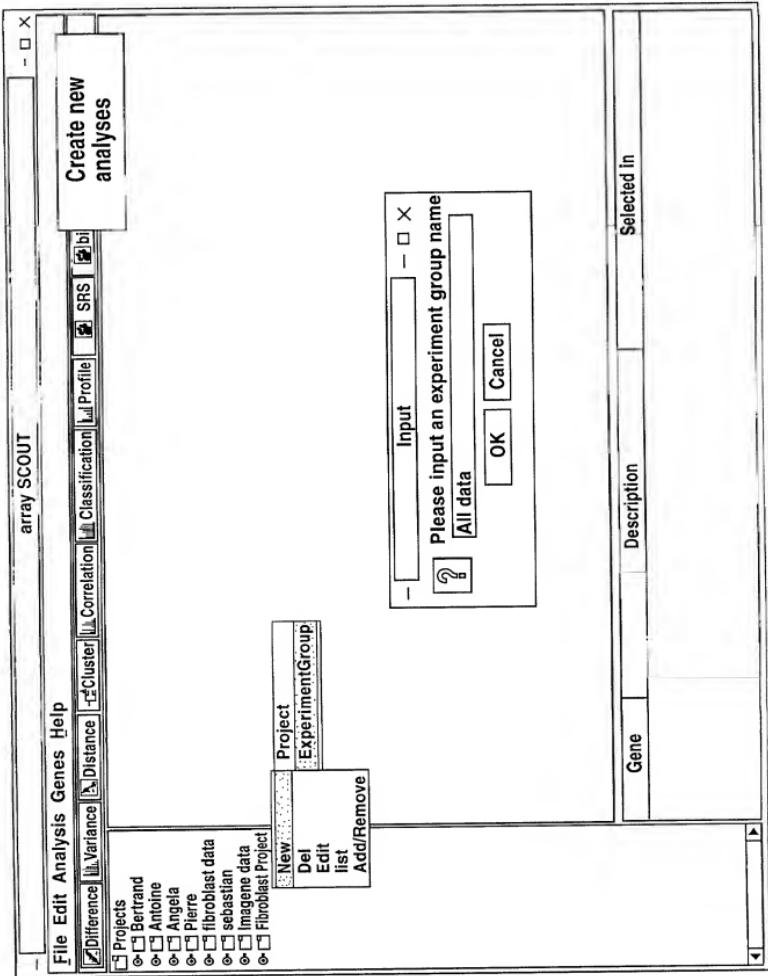


FIG.62

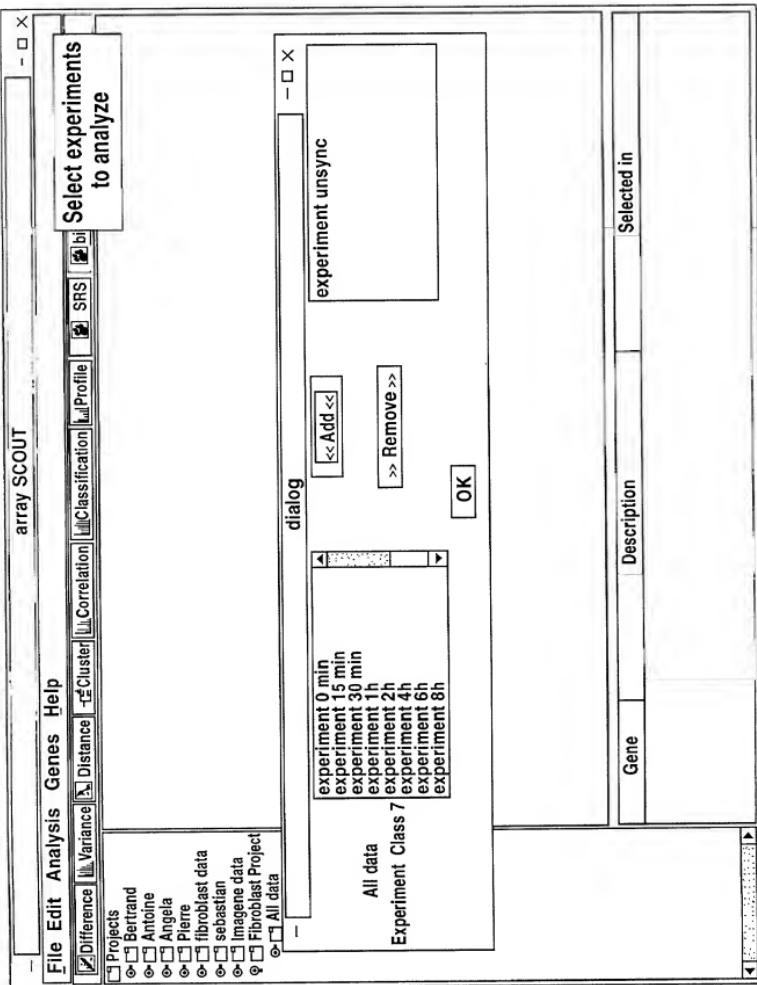


FIG.63

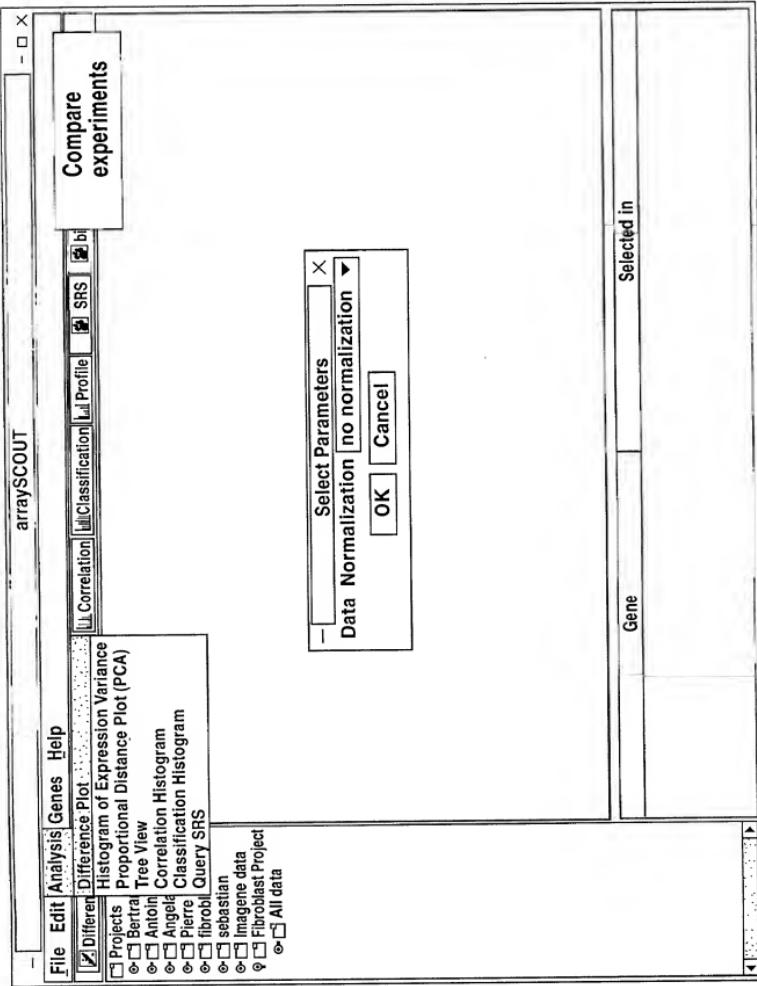


FIG. 64

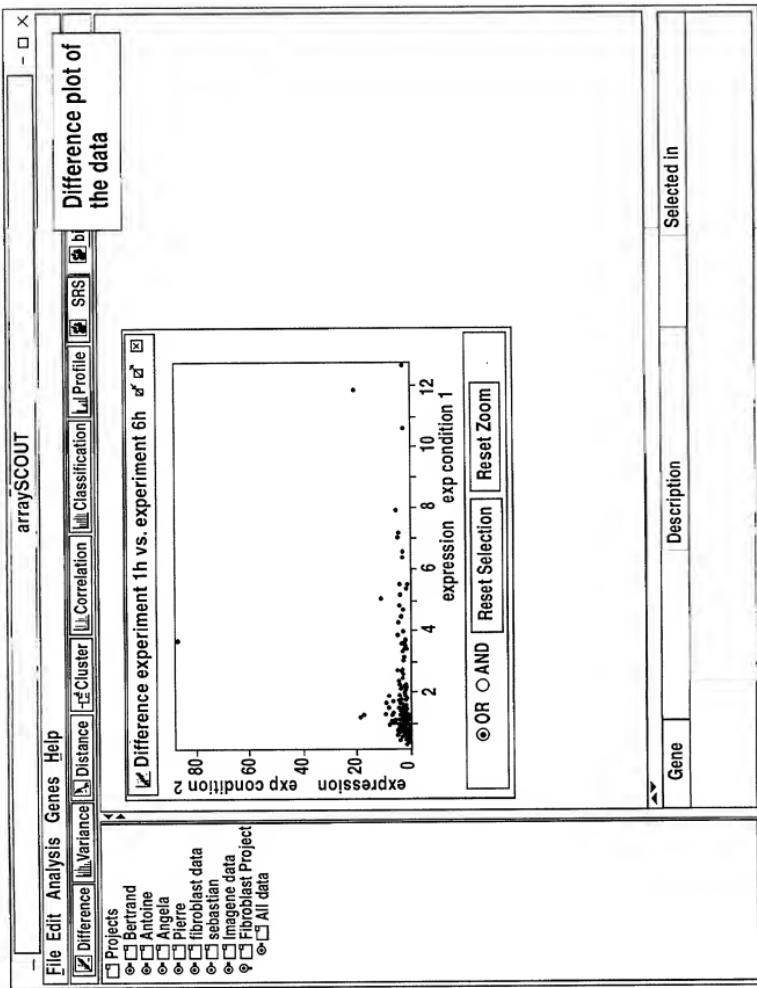


FIG.65

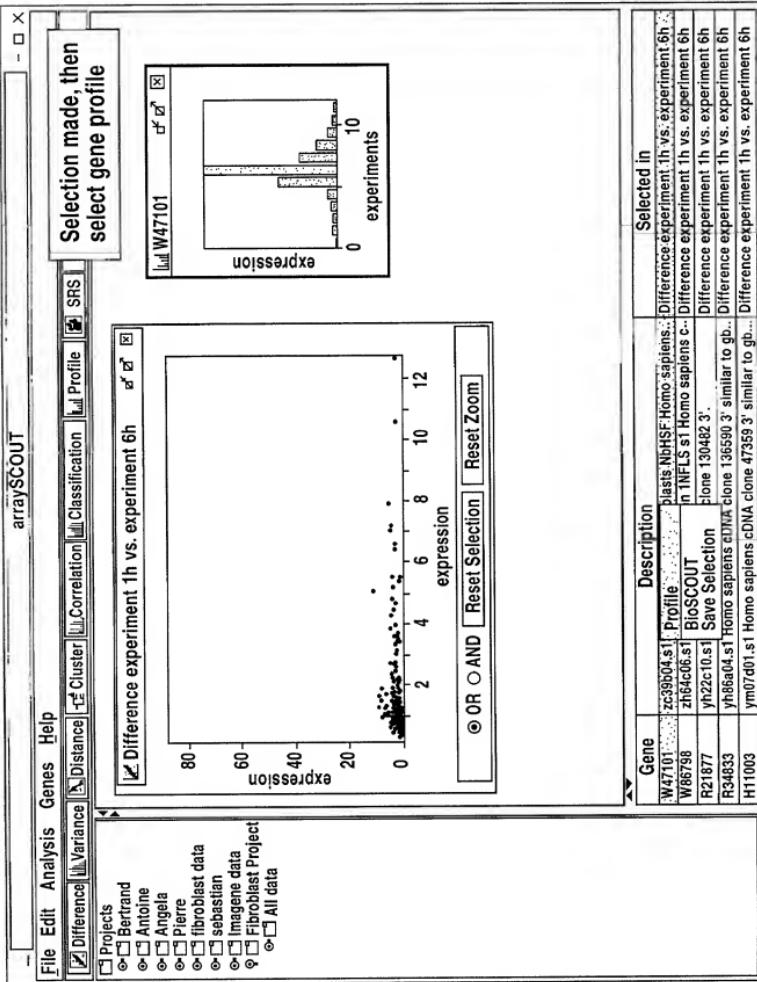
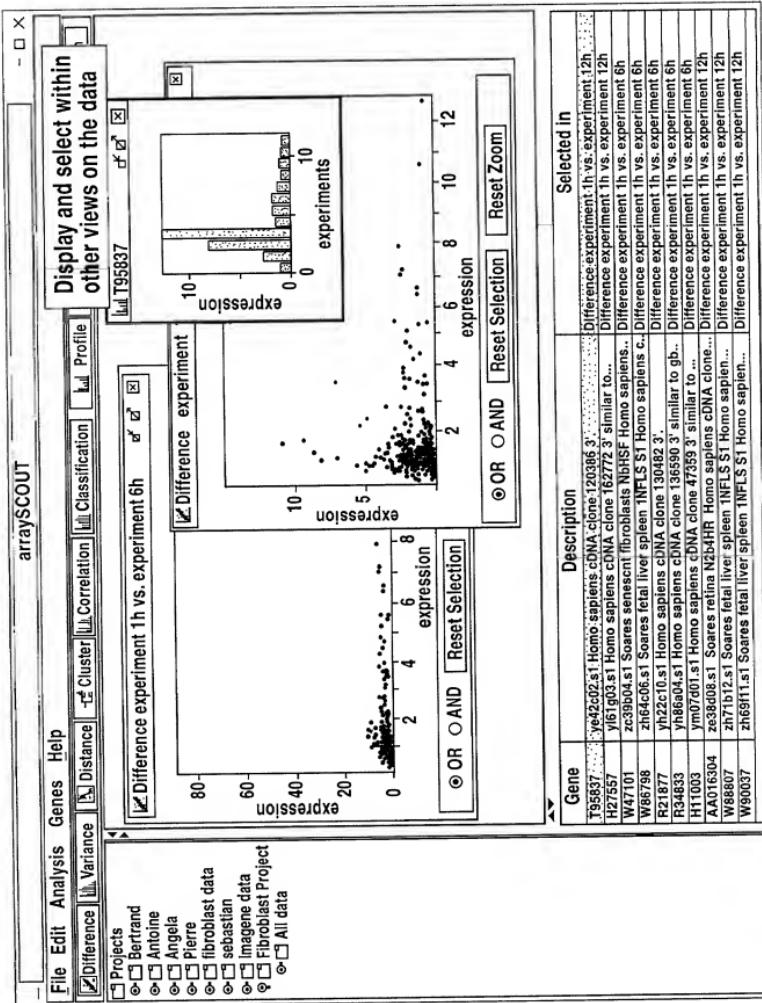
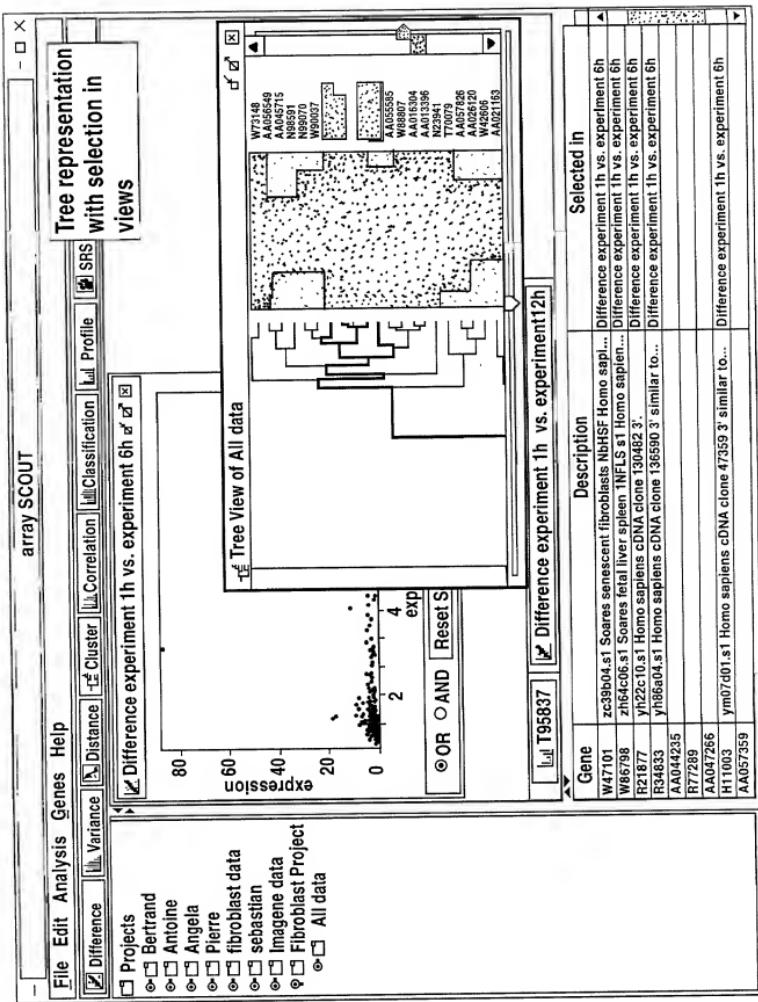
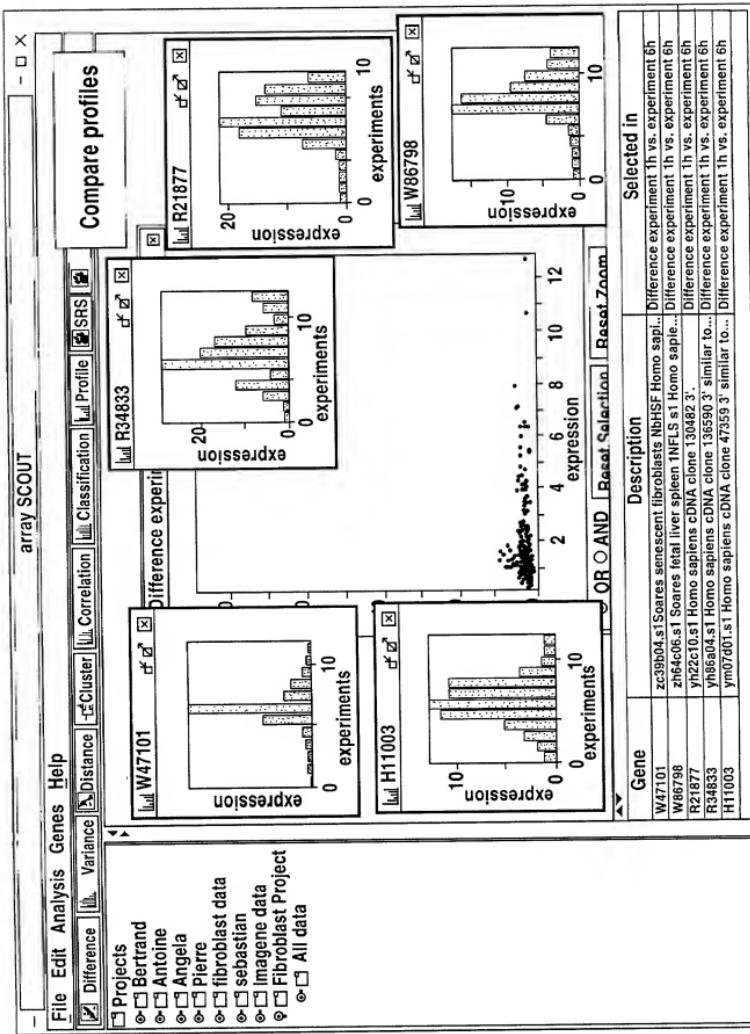


FIG.66

FIG. 67



**FIG. 68**



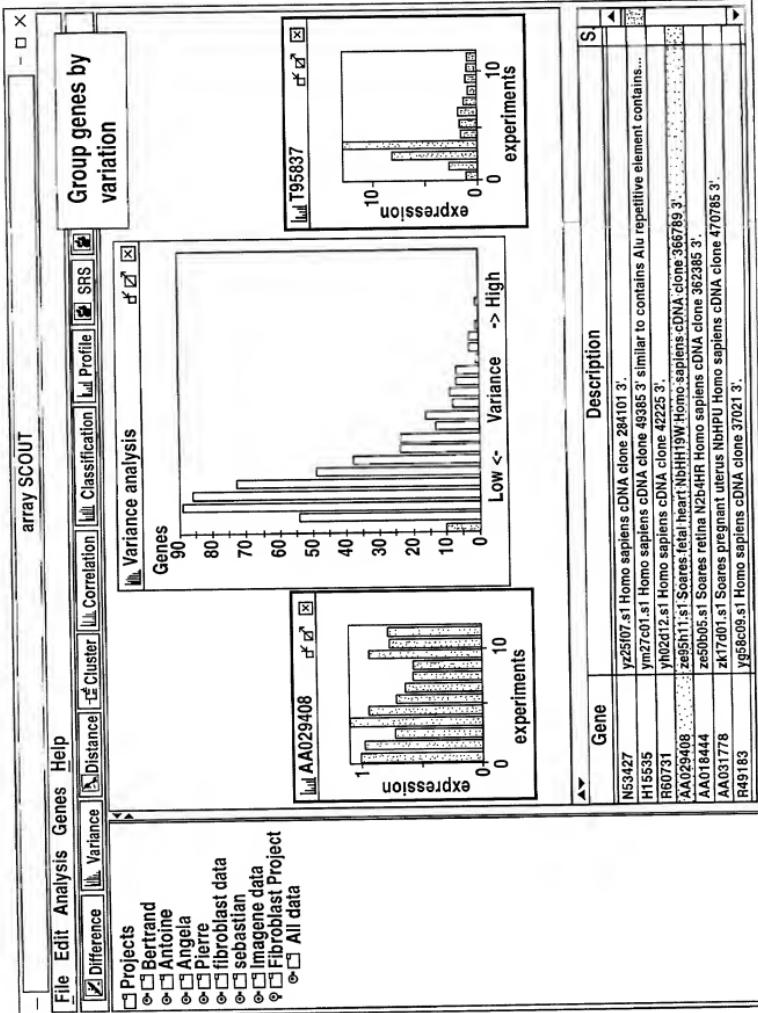
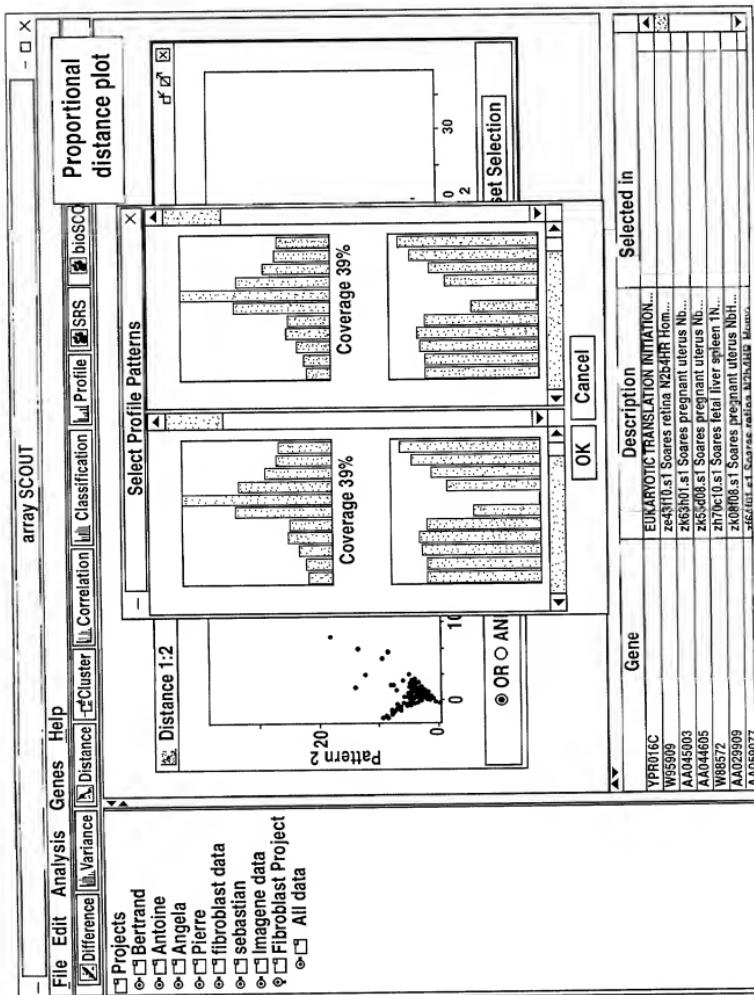


FIG.70



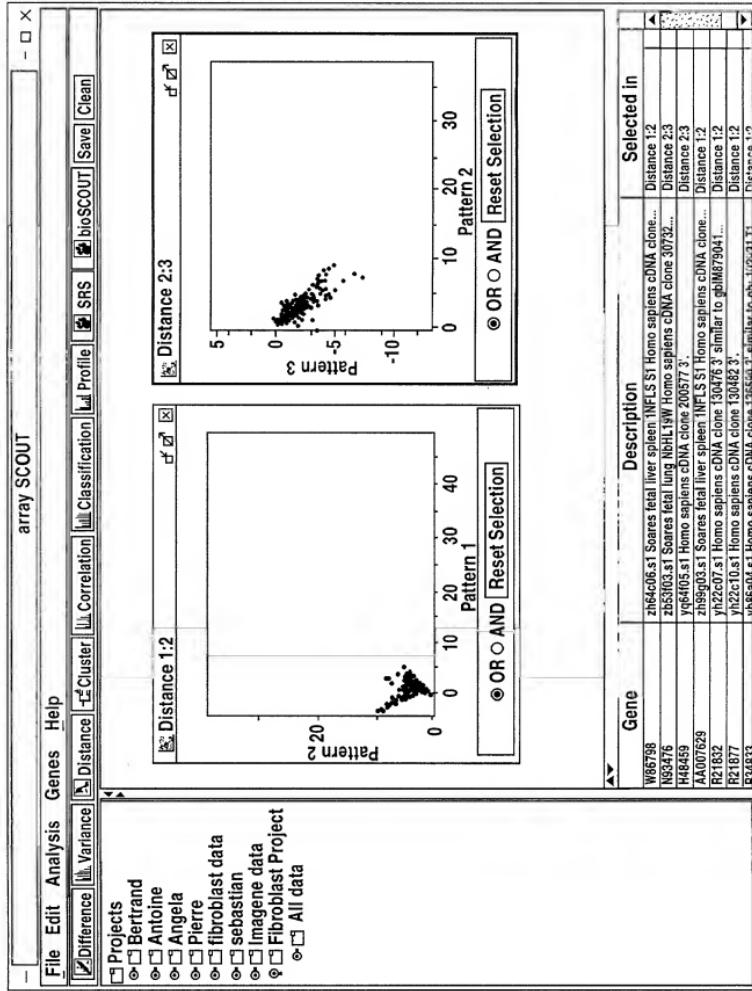
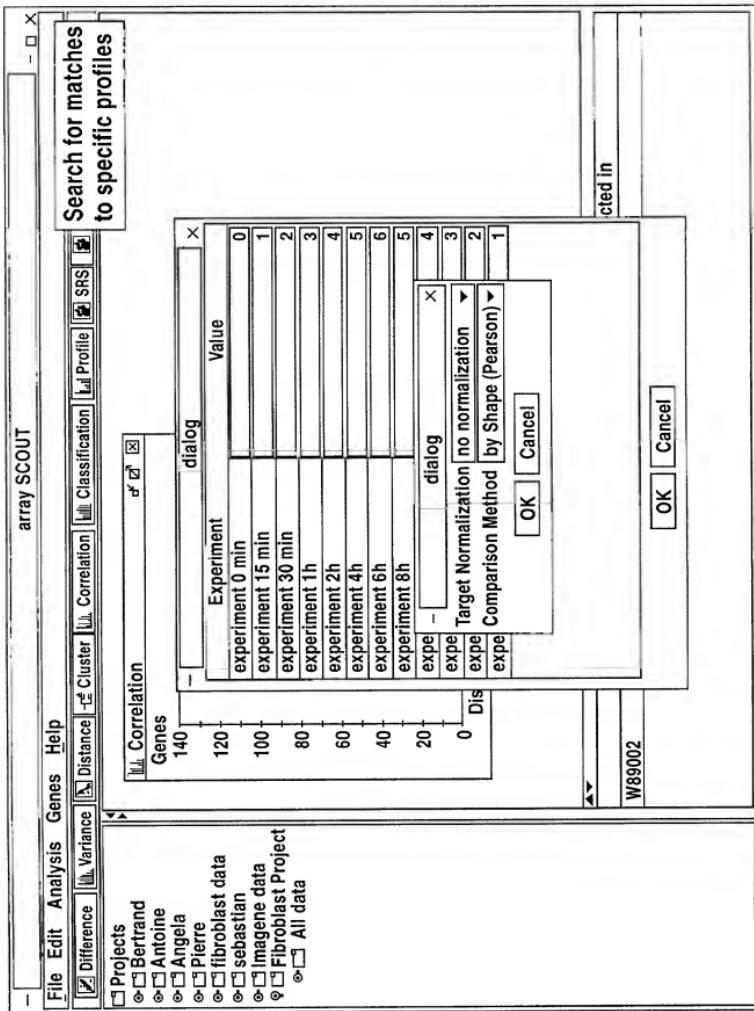


FIG. 72



**FIG.73**

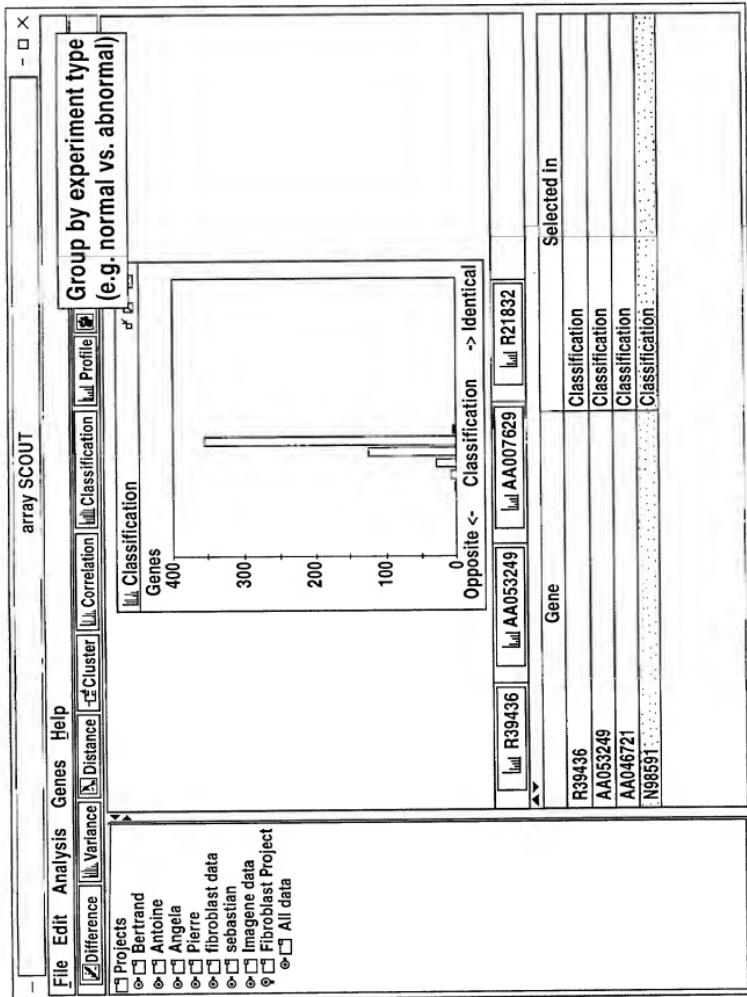


FIG.74

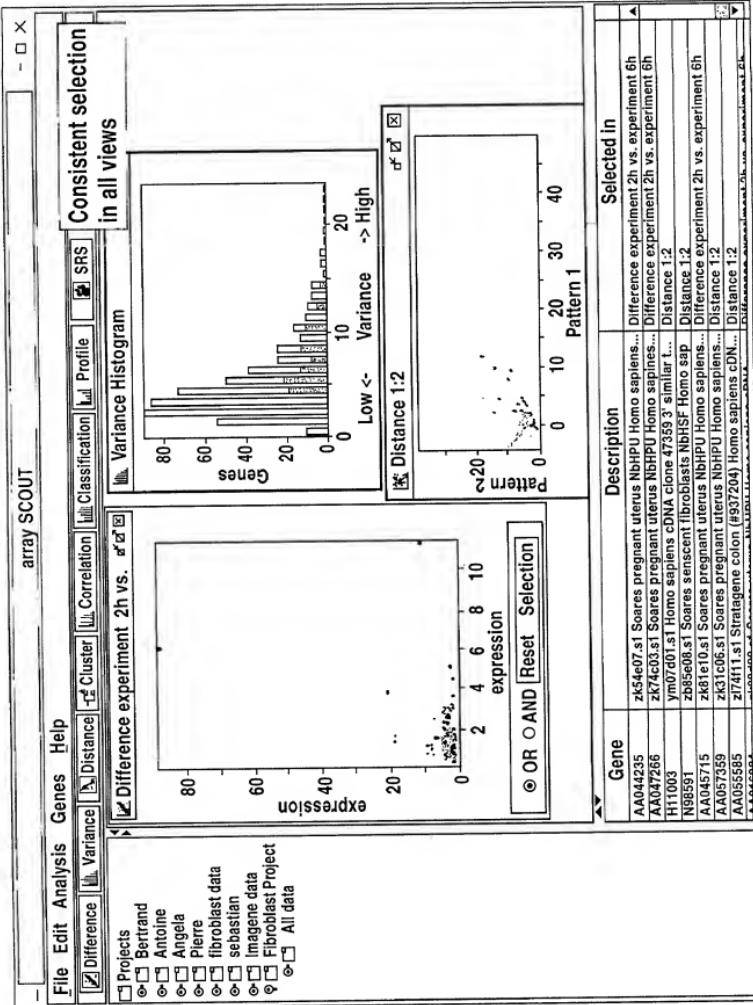
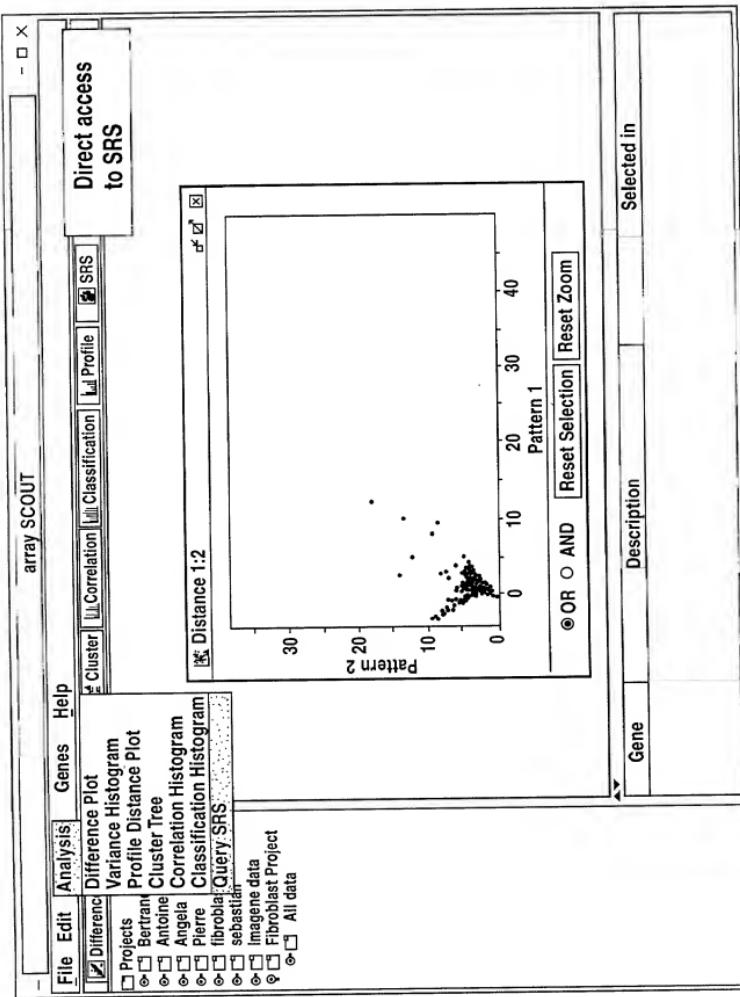


FIG.75

FIG. 76



- □ ×

array SCOUT

**SRS queries can be easily constructed using this interface**

File Edit Analysis Genes Help

Difference Variance Distance Cluster Correlation Classification Profile SRS

Projects Bertrand Antoine Angela Pierre sebastian fibroblast data Imagine data Fibroblast Project All data

SRS Stop Simple mode Submit Deselect + - Q1 all dbs SacRelated Protein3Struct Sequence Mutations TransFac Mapping Metabolic Pathways Others

Back Forward

Gene	Description	Selected in
W86786	rb6d6.s1 Sonote fetal liver spleen INFSL...	Distance 1:2
R21877	yh22t0.s1 Homo sapiens cDNA clone 130...	Distance 1:2
R34853	yh6840.s1 Homo sapiens cDNA clone 136...	Distance 1:2
H1063	ym7dg1.s1 Homo sapiens cDNA clone 47...	Distance 1:2

FIG.77

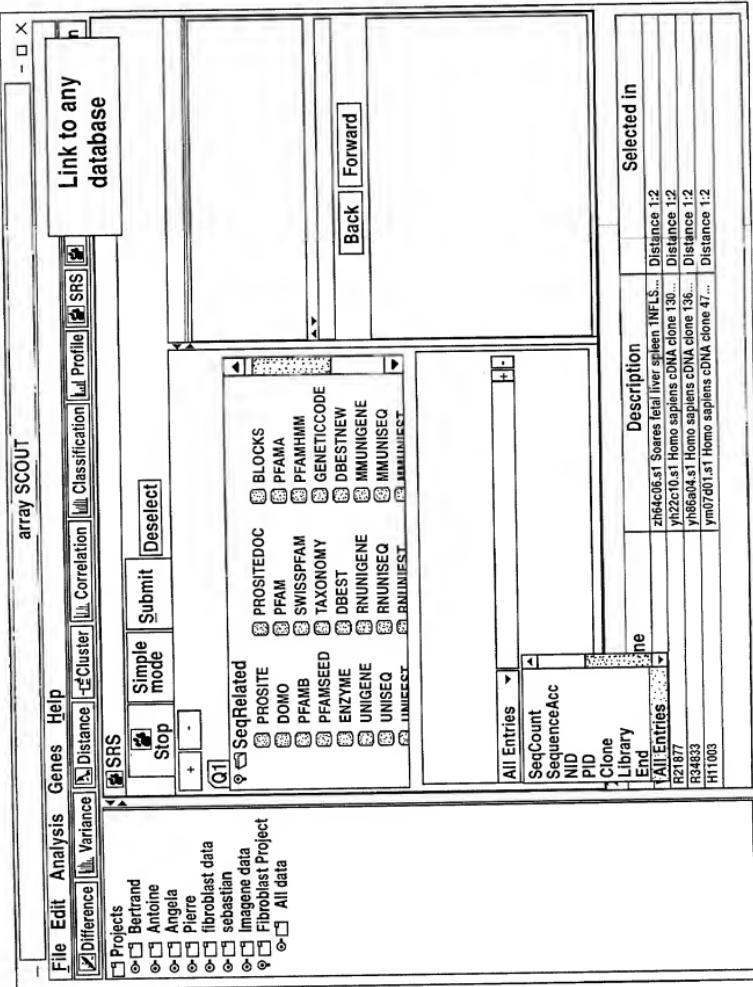


FIG.78

array SCOUT

Link again for specific query e.g. cytokine

File Edit Analysis Genes Help

Difference Variance

Projects

- Bertrand
- Antoine
- Angela
- Pierre
- fibroblast data
- sebastian
- Imagine data
- Fibroblast Project
- All data

SRS

Distance Cluster Correlation Classification Profile SRS

Simple Mode Stop Submit Deselect

Q1 > Q2 SeqRelated Protein3DStruct Sequence

EMBL NEW GENBANK SWISSPROT SPTRREMBL GENPEPT GENPEPT NEW

EMBL GENBANK NEW SWISSPROT SPTRREMBL GENPEPT GENPEPT NEW

PIR TREMBLNEW TREMBL SPTRREMBL AAGENESEO NEW

ALTText → cytokine +

Selected in

Gene	Description
W86798	zr6e06_s1 Scores leish liver against 1NF.L... Distance 1:2
R21877	yf22e07_s1 Homo sapiens cDNA clone [30... Distance 1:2
R34833	yf18e04_s1 Homo sapiens cDNA clone [36... Distance 1:2
H11003	ym07d01_s1 Homo sapiens cDNA clone [47... Distance 1:2

FIG.79

array SCOUT

**Results displayed**

File Edit Analysis Genes Help

Difference Variance Distance t<sup>2</sup> Cluster Correlation Classification LProfile SRS

Projects Bertrand Antoine Aligela Pierre fibroblast data sebastien Imagene data Fibroblast Project All data

SRS Stop Simple mode Submit Deselect

Q1 > Q2 SeqRelated Protein3DStruct Sequence EMBL GENBANKNEW SWISSPIR PIR TREMBLNEW GEN TREMBL SPTR

function subgff(form,addEl) {form.elements[form.elements.length-1].value = "View";}

\* Complete entries\*

SWISSPROT:SY02\_HUMAN

ID	SY02_HUMAN STANDARD	PRT;	99 AA.
AC	P13500;		
DT	01~JAN~1990	(Rel. 13, Created)	
	01~JUL~1990	(Rel. 13, Last sequence update)	
	15~JUL~1999	(Rel. 38, Last annotation update)	

AllText cytokine

Gene Description Selected In

T7787 ... 1cd2011.s1 Homo sapiens cDNA clone 67/... Distance 1.2...

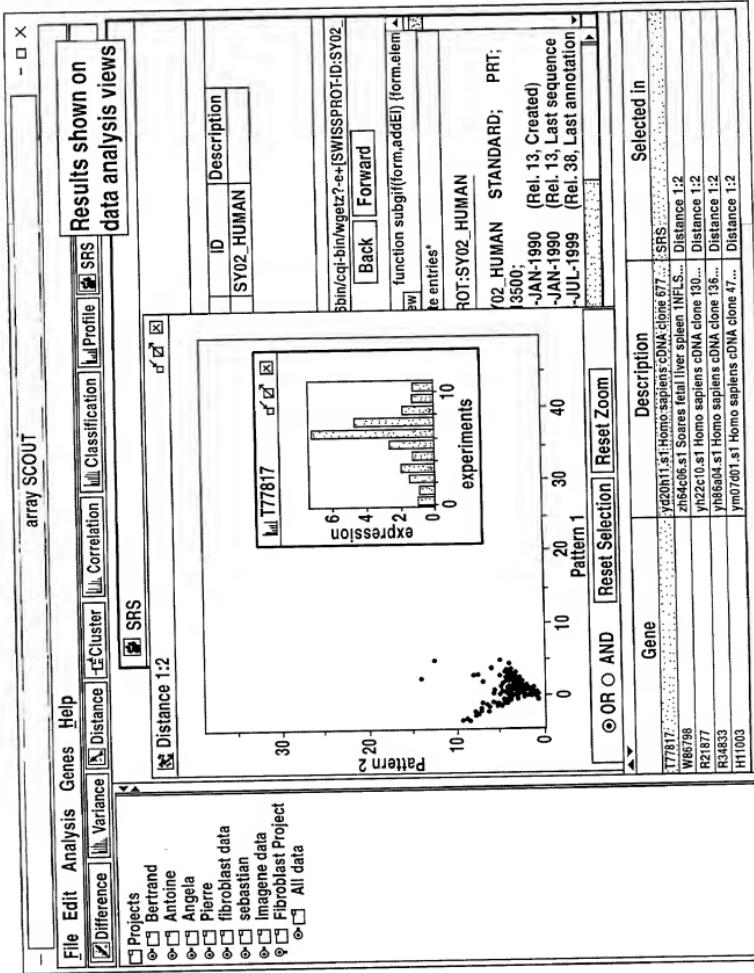
W85738 ... 2hb4406.s1 Seraes fetal liver spleen INFSL... Distance 1.2...

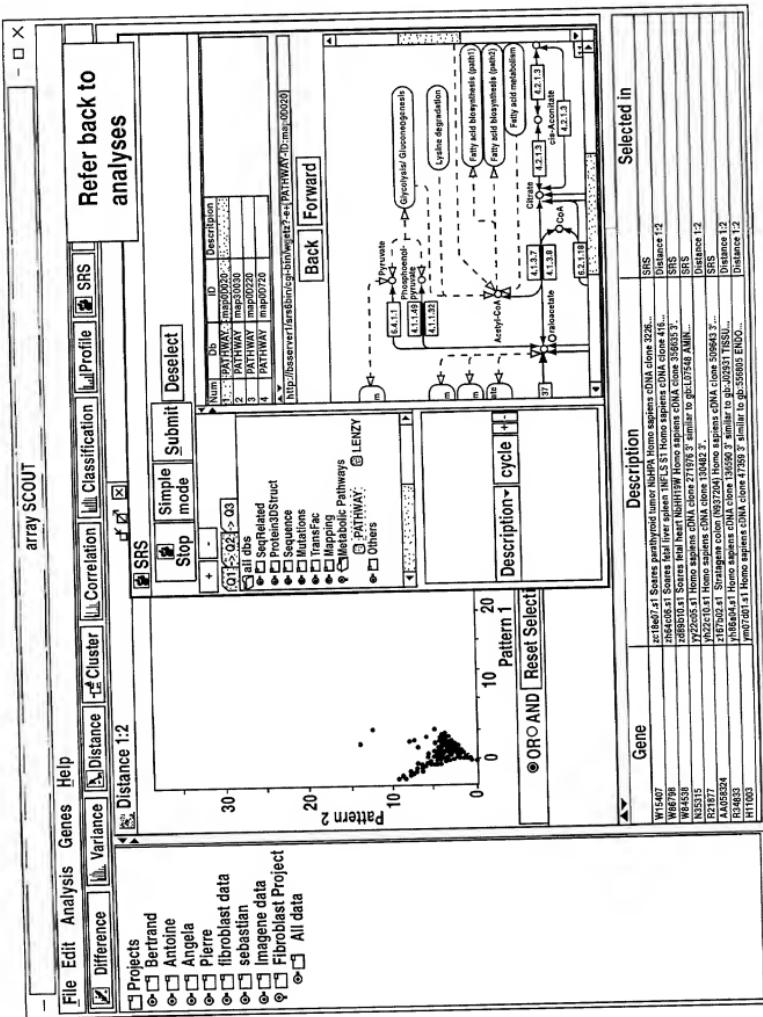
R21877 ... 1hf2210.s1 Homo sapiens cDNA clone 130... Distance 1.2...

B34823 ... 1yb6504.s1 Homo sapiens cDNA clone 136... Distance 1.2...

H11063 ... 1ym07d01.s1 Homo sapiens cDNA clone 41... Distance 1.2...

FIG.80





**FIG.82**

FIG. 83

